SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

<130> 896034605001
<140> US 09/966,264
<141> 2001-09-28

<150> US 60/237,079
<151> 2000-09-30

<160> 61

<170> PatentIn version 3.1

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   Tyr Lys Gly Lys Arg Lys     Arg Asn Gly Gln Val Val Lys Leu
   1               5                       10

tga act cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga 95
    Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
    15                  20                  25

ggt aga aat agc atg aga agc cgt gtt tga tgt taa tta att        137
Gly Arg Asn Ser Met Arg Ser Arg Val     Cys     Leu Ile
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Val Val     Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
    Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
                    20                  25                  30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
                35                  40                  45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192
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Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala     His
            50                  55                  60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
Phe Ser Met     Thr Pro Val Ala     Ser Asn Ile Lys Leu Ile Leu
                65                      70                  75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
Thr Asn Asn Val     Trp Leu His         Gly Phe Ala Ser Ser Trp
                    80                          85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
    90                  95                  100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
105                 110                 115                 120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
Glu Thr Glu     Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
                    125                 130                 135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
                140                 145                 150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
            155                 160                 165

gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
Asp Glu Glu Gly Ala Glu     Met Phe Tyr Asn Ser     Phe Pro His
        170                     175                     180

ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln     Glu Phe
            185                 190                     195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
Thr Arg Asn Lys Ser Ile Phe Leu     Arg Val Val Val Leu Tyr Cys
            200                     205                 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
Arg Phe Gln     Phe Leu Ser Leu Leu Leu Phe Cys     Gln Trp Gln
                215                 220                     225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
                230                 235                 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
Cys Lys Ile Leu Ile Ala Lys     Leu Ala Ile Ser Leu Tyr Gly Thr
            245                     250                 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
His Phe Gly Leu Phe Lys Asn Leu     Gln Leu     Arg Lys Asn Tyr
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            260                 265                 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
Lys Gly Lys Arg Lys     Arg Asn Gly Gln Val Val Lys Leu     Thr
                275                 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys     Gly Arg
285                 290                 295

aat agc atg aga agc cgt gtt tga tgt taa tta att                 996
Asn Ser Met Arg Ser Arg Val     Cys     Leu Ile
300                 305
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<210> 4
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<400> 4

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1               5                   10
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<211> 18
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Glu Glu
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ggaaaagact tccacattgt 20

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<210> 14
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<223> histone methylation site

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<223> histone methylation site

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<400> 15
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gccaaggtgg aaaagatg 18

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ccagtagcct gatccaac 18

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ggcttcatta ataag 15

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ggcaaagaaa cagagtg 17

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caggacacaa tgtagga 17

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<400> 21
gttataaaga aagaattata aag 23

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ctttttcctt tataattctt tc 22

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Met Phe Val Asn Thr Thr Lys Val Glu Lys Met Tyr Pro Ile Met Glu
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Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu
            20                  25                  30

Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys
        35                  40                  45

Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln
    50                  55                  60

Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe
65                  70                  75                  80

Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg
                85                  90                  95

Lys Leu His Lys Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser
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Glu Val Glu Ile Ala
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<223> Putative membrane-spanning segment

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<223> Putative membrane-spanning segment

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Ala Lys Val Glu Lys Met Tyr Pro Ile Met Glu Tyr Ser Cys Ser Asp
            20                  25                  30

Arg Asn Leu Val Leu Ile Tyr Gly Ile Leu Leu Ile Tyr Ile Tyr Ile
        35                  40                  45

Gly Asn Leu Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala
    50                  55                  60

Arg Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His
65                  70                  75                  80

Lys Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
                85                  90                  95

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
            100                 105                 110

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr Leu Ser
        115                 120                 125

Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe Pro Gly His
    130                 135                 140

Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu Gly Arg Ala Met
145                 150                 155                 160

Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu Gly Ala Glu Lys Met
                165                 170                 175

Phe Tyr Asn Ser Arg Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr
            180                 185                 190

Lys Arg Ile Arg Gln Lys Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
        195                 200                 205

Arg Arg Val Val Val Leu Tyr Cys Arg Phe Gln Lys Phe Leu Ser Leu
    210                 215                 220

Leu Leu Phe Cys Lys Gln Trp Gln Val Leu His Val Tyr Ala Ile Val
225                 230                 235                 240

Gln Lys Ser Tyr Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys
                245                 250                 255

Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
            260                 265                 270

Lys Gln Leu Lys Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn
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        275                 280                 285

Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
    290                 295                 300

Thr Pro Lys Pro Lys Arg Gly Arg Asn Ser Met Arg Ser Arg Val Arg
305                 310                 315                 320

Cys Lys Leu Ile
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<210> 33
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1               5                   10                  15

att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc  96
Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
            20                  25                  30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
        35                  40                  45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
        50                  55                  60

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg         234
Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met
    65                  70                  75
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<210> 34
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<213> human

<400> 34

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Tyr Lys Gly Lys Arg Lys
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<210> 35
<211> 8
<212> PRT
<213> human

<400> 35

Arg Asn Gly Gln Val Val Lys Leu
1 5

<210> 36
<211> 14
<212> PRT
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<400> 36

Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
1 5 10

<210> 37
<211> 9
<212> PRT
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Gly Arg Asn Ser Met Arg Ser Arg Val
1 5

<210> 38
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Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1 5 10

<210> 39
<211> 45
<212> PRT
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<400> 39

Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
1 5 10 15

Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr

20 25 30

Gly Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala
35 40 45

<210> 40
<211> 11
<212> PRT
<213> human

<400> 40
Ser Asn Ile Lys Leu Ile Leu Thr Asn Asn Val
1 5 10

<210> 41
<211> 41
<212> PRT
<213> human

<400> 41

Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu Leu
1 5 10 15

Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu Met
20 25 30

Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu
35 40

<210> 42
<211> 50
<212> PRT
<213> human

<400> 42

Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu
1 5 10 15

Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp
20 25 30

Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
35 40 45

Glu Glu Gly Ala Glu
50

<210> 43
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<212> PRT
<213> human

<400> 43

Met Phe Tyr Asn Ser
1 5

<210> 44
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<212> PRT
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<400> 44

Phe Pro His Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln
1 5 10 15

<210> 45
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<212> PRT
<213> human

<400> 45

Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
1 5 10

<210> 46
<211> 10
<212> PRT
<213> human

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Arg Val Val Val Leu Tyr Cys Arg Phe Gln
1 5 10

<210> 47
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<212> PRT
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<400> 47

Phe Leu Ser Leu Leu Leu Phe Cys
1 5

<210> 48
<211> 26
<212> PRT
<213> human

<400> 48

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Gln Trp Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr
1               5                   10                  15

Lys Lys Thr Thr Cys Lys Ile Leu Ile Ala Lys
                20                  25
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<210> 49
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<213> human

<400> 49

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Leu Ala Ile Ser Leu Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu
1               5                   10                  15
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<210> 50
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<212> PRT
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<400> 50

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Arg Lys Asn Tyr Lys Gly Lys Arg Lys
1               5
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<210> 51
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<212> DNA
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<400> 51

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            -75                 -70                 -65

ttt att att att att ttc aac cca agt aaa agc aga gag aaa ata gcc -144
Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
            -60                 -55                 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg -96
Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu
        -45                 -40                 -35

aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc -48
Lys     Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr
        -30                 -25                 -20

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg gat ggt  0
Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met Asp Gly
    -15                 -10                 -5
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gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag  48
Val Val     Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu
1                   5                  10                  15

taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc  96
    Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
                20                  25                  30

atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
            35                  40                  45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192
Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala     His
        50                  55                  60

ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
Phe Ser Met     Thr Pro Val Ala     Ser Asn Ile Lys Leu Ile Leu
            65                  70                  75

aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
Thr Asn Asn Val     Trp Leu His         Gly Phe Ala Ser Ser Trp
                80                  85

aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
    90                  95                  100

ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
105                 110                 115                 120

gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
Glu Thr Glu     Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
                125                 130                 135

ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
            140                 145                 150

gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
        155                 160                 165

gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
Asp Glu Glu Gly Ala Glu     Met Phe Tyr Asn Ser     Phe Pro His
    170                 175                 180

ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln     Glu Phe
            185                 190                 195

aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
Thr Arg Asn Lys Ser Ile Phe Leu     Arg Val Val Val Leu Tyr Cys
        200                 205                 210

aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
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Arg Phe Gln     Phe Leu Ser Leu Leu Leu Phe Cys     Gln Trp Gln
                215                 220                 225

gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
                230                 235                 240

tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
Cys Lys Ile Leu Ile Ala Lys     Leu Ala Ile Ser Leu Tyr Gly Thr
            245                     250                 255

cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
His Phe Gly Leu Phe Lys Asn Leu     Gln Leu     Arg Lys Asn Tyr
            260                     265                 270

aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
Lys Gly Lys Arg Lys     Arg Asn Gly Gln Val Val Lys Leu     Thr
                275                 280

cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys     Gly Arg
285                 290                 295

aat agc atg aga agc cgt gtt tga tgt taa tta att                 996
Asn Ser Met Arg Ser Arg Val     Cys     Leu Ile
300                 305
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<210> 52
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<212> PRT
<213> human

<400> 52

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Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe
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Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
                20                  25                  30

Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala
                35                  40                  45

Leu Lys
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<210> 53
<211> 32
<212> PRT
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<400> 53

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Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp
1               5                   10                  15
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Gly Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met
20 25 30

Val Val

<210> 54
<211> 1044
<212> DNA
<213> mouse

<400> 54

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actgtgctgg taatggtgat cttagcaggc agagaaggtg gtagtgattt 100

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ccaacaaagt gtgaaaggtg tgtgccatta cacatctttc tcggtgataa 200

gagccttgtc tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250

ttacatttct ccccatcaaa tgacaccatg ctgatccagt attaagctaa 300

tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350

atgggtaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400

tgtcttttcc tgaaatggta atgactccca atagtggcaa ccaggggtac 450

aatacttgca cactttgtaa actctttctt tctctttgtt ttccaggaca 500

caatgtagga agccttttcc acatggcaga tgatttgggc agagcgatgg 550

agtccttagt ttcagtcatg acagatgaag aaggagcaga ataaatgttt 600

tacaactcct gattcccgca tggtttttat aatattcgta caacaaagag 650

gattagacag taagagttta caagaaataa aatctatatt tttgtgaagg 700

gtagtggtac tatactgtag atttcagtag tttctaagtc tgttattgtt 750

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aaaagaaaac atgtaaaatc ttgatagcta aataacttgc catttcttta 850

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gattgtaaac taaagtgtgc tttataaaaa aagttgttta taaaaacccc 950

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tgctggtgat ggtagtggta gttgtga.ag gtggtgatgg tggtttgatt 250

gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc 300

aatcactcat agccaaggtg gaaaagatgt atcccatcat ggaatattcc 350

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Asn Val Ala Arg His Phe Ser Met Lys Thr Pro Val Ala Arg Ser
        35                  40                  45

Asn Ile Lys Leu Ile Leu Thr Asn Asn Val Lys Trp Leu His Lys
    50                  55                  60

Lys Gly Phe Ala Ser Ser Trp Lys Leu Val Lys Asn Gln Thr Leu
65                  70                  75

Leu Cys Thr Pro Ser Met Gln Leu Leu Cys Cys Leu His Pro Glu
                80                  85                  90

Met Gly Asn Asp Phe Pro Asn Gly Lys Glu Thr Glu Arg Cys Tyr
            95                  100                 105

Leu Ser Ala Pro Phe Val Lys Ser Val Phe Leu Ser Leu Cys Phe
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Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp Asp Leu
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Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp Glu Glu
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Gly Ala Glu Lys Met Phe Tyr Asn Ser Arg Phe Pro His Gly Phe
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Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln Lys Glu Phe Thr
        170                 175                 180

Arg Asn Lys Ser Ile Phe Leu Arg Arg Val Val Val Leu Tyr Cys
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Arg Phe Gln Lys Phe Leu Ser Leu Leu Leu Phe Cys Lys Gln Trp
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Gln Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys
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Thr Thr Cys Lys Ile Leu Ile Ala Lys Lys Leu Ala Ile Ser Leu
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Tyr Gly Thr His Phe Gly Leu Phe Lys Asn Leu Lys Gln Leu Lys
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Arg Lys Asn Tyr Lys Gly Lys Arg Lys Lys Arg Asn Gly Gln Val
260 265 270

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Lys Leu Ile

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gcggtgatgg tggcagt 17

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<400> 61

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35 40 45

Arg Met Val Phe Ile Ile Phe Ile Gln Gln Arg Gly Leu Asp Ser
50 55 60

Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe Cys Glu Gly Phe Tyr
65 70 75

Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg Lys Leu His Lys
80 85 90

Ile Thr Gln Trp Thr Arg Thr Pro Gln Asn Gln Ser Glu Val Glu

95 100 105

Ile Ala